

SEQUENCE LISTING

<110> GIMENO, Ruth

<120> METHODS FOR THE TREATMENT OF METABOLIC DISORDERS, INCLUDING OBESITY AND DIABETES

<130> MNI-220

<150> 60/271, 655

<151> 2001-02-26

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1743

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (44)...(1129)

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Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser Leu Glu Gln Ala
5 10 15 20

aac cgc acc cgc ttt ccc ttc ttc tcc gac gtc aag ggc gac cac cgg 151
Asn Arg Thr Arg Phe Pro Phe Ser Asp Val Lys Gly Asp His Arg
25 30 35

ctg gtg ctg gcc gcg gtg gag aca acc gtg ctg gtg ctc atc ttt gca 199
Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val Leu Ile Phe Ala
40 45 50

gtg tcg ctg ctg ggc aac gtg tgc gcc ctg gtg ctg gtg gcg cgc cga 247
Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu Val Ala Arg Arg
55 60 65

cga cgc cgc ggc gcg act gcc tgc ctg gta ctc aac ctc ttc tgc gcg 295
Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn Leu Phe Cys Ala
70 75 80

gac ctg ctc ttc atc agc gct atc cct ctg gtg ctg gcc gtg cgc tgg 343
Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu Ala Val Arg Trp
85 90 95 100

act gag gcc tgg ctg ctg ggccccc gtt gcc tgc cac ctg ctc ttc tac 391
Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His Leu Leu Phe Tyr
105 110 115

gtg atg acc ctg agc ggc agc gtc acc atc ctc acg ctg gcc gcg gtc 439
Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr Leu Ala Ala Val

120	125	130	
agc ctg gag cgc atg gtg tgc atc gtg cac ctg cag cgc ggc gtg cg			487
Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln Arg Gly Val Arg			
135	140	145	
ggc cct ggg cgg cg gcg cgg gca gtg ctg ctg gcg ctc atc tgg ggc			535
Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala Leu Ile Trp Gly			
150	155	160	
tat tcg gcg gtc gcc gct ctg cct ctc tgc gtc ttc ttt cga gtc gtc			583
Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe Phe Arg Val Val			
165	170	175	180
ccg caa cgg ctc ccc ggc gcc gac cag gaa att tcg att tgc aca ctg			631
Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser Ile Cys Thr Leu			
185	190	195	
att tgg ccc acc att cct gga gag atc tcg tgg gat gtc tct ttt gtt			679
Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp Val Ser Phe Val			
200	205	210	
act ttg aac ttc ttg gtg cca gga ctg gtc att gtg atc agt tac tcc			727
Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val Ile Ser Tyr Ser			
215	220	225	
aaa att tta cag atc aca aag gca tca agg aag agg ctc acg gta agc			775
Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg Leu Thr Val Ser			
230	235	240	
ctg gcc tac tcg gag agc cac cag atc cgc gtg tcc cag cag gac ttc			823
Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser Gln Gln Asp Phe			
245	250	255	260
cgc ctc ttc cgc acc ctc ttc ctc atg gtc tcc ttc ttc atc atg			871
Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser Phe Phe Ile Met			
265	270	275	
tgg agc ccc atc atc acc atc ctc ctc atc ctg atc cag aac ttc			919
Trp Ser Pro Ile Ile Thr Ile Leu Leu Ile Leu Ile Gln Asn Phe			
280	285	290	
aag caa gac ctg atc tgg ccg tcc ctc ttc tgg gtg gtg gcc			967
Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe Trp Val Val Ala			
295	300	305	
ttc aca ttt gct aat tca gcc cta aac ccc atc ctc tac aac atg aca			1015
Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu Tyr Asn Met Thr			
310	315	320	
ctg tgc agg aat gag tgg aag aaa att ttt tgc tgc ttc tgg ttc cca			1063
Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys Phe Trp Phe Pro			
325	330	335	340
gaa aag gga gcc att tta aca gac aca tct gtc aaa aga aat gac ttg			1111
Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys Arg Asn Asp Leu			
345	350	355	
tcg att att tct ggc taa tttttcttta tagccgagtt tctcacac			1159
Ser Ile Ile Ser Gly *			
360			

ggcagctgt ggcattttttt taaacagagt tcattccat taccctccat cagtgcaccc 1219
 tgcttaaga aaatgaacct atgcaaatag acatccacag cgtcggtaaa ttaagggtg 1279
 atcaccaagt ttccataatat ttcccttta taaaaggatt tttggccag gtgcagtgg 1339
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 gttcgagacc aacctgacca acatggtag acccccgtct ctactaaaaaa taaaaaaaaa 1459
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 caaccaggc aacaagagtg aaactccatc taaaaaaaaa aaaaaaaaaaag atttgttatg 1639
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<210> 2
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 <212> PRT
 <213> Homo sapiens

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 Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
 20 25 30
 Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
 35 40 45
 Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
 50 55 60
 Val Ala Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
 65 70 75 80
 Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
 85 90 95
 Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
 100 105 110
 Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
 115 120 125
 Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
 130 135 140
 Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
 145 150 155 160
 Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
 165 170 175
 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
 180 185 190
 Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
 195 200 205
 Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
 210 215 220
 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
 225 230 235 240
 Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
 245 250 255
 Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
 260 265 270
 Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Ile Leu
 275 280 285
 Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
 290 295 300
 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
 305 310 315 320
 Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
 325 330 335
 Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys

350

340	345	
Arg Asn Asp Leu Ser Ile Ile Ser Gly		
355	360	

<210> 3
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<212> DNA
<213> Homo sapiens

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gcggtgtggaga caaccgtgct ggtgctcatc tttgcagtgt cgctgctggg caacgtgtgc 180
gcctctggc tggtggcgcg ccgacgcgcg cgcggcgca ctgcctgcct ggtactcaac 240
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actgaggcct ggctgctggg ccccggttgc tgccacctgc tcttctacgt gatgaccctg 360
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gtgcacccgtc agcgcggcggt gcgggggtcct gggcgccggg cgcgggcagt gctgctggcg 480
ctcatctggg gctattcgcc ggtcgccgct ctgcctctct gcgtcttctt tcgagtcgtc 540
ccgcaacggc tccccggcgc cgaccaggaa atttcgattt gcacactgtat ttggcccacc 600
attcctggag agatctcgat gatatgtctt tttgttaatt tgaacttctt ggtgccagga 660
ctggtcattt tgatcagttt ctccaaaattt ttacagatca caaaggcatc aaggaagagg 720
ctcacggtaa gcctggccta ctccggagagc caccagatcc gcgtgtccca gcaggacttc 780
cggtcttcc gcaccctctt ctcctcatg gtctcttct tcatacatgtg gagccccatc 840
atcatcacca tcctccatcat cctgatccag aactcaagc aagaccttggt catctggccg 900
tcctctttct tctgggtggt ggccttcaca tttgtaattt cagccctaaa ccccatccctc 960
tacaacatga cactgtgcag gaatgagttt aagaaaattt tttgctgctt ctggttccca 1020
gaaaaggag ccatttaac agacacatct gtcaaaaagaa atgacttgatc gattatttct 1080
ggctaa 1086

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<213> Murine ortholog

<220>
<221> CDS
<222> (195)...(1280)

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ttcacaccat cagtgaccac tccagacttg tccgcttta cccgaatctt cacagcgag 120
tcgatgaccc tcttgacagc cacgagcgcg cgcaagctccg ccatcttccc ggacgcgtgg 180
gccggcgcc cggc atg tcc cct gag tgt gca cag acg acg ggc cct ggt 230
Met Ser Pro Glu Cys Ala Gln Thr Thr Gly Pro Gly
1 5 10

ccc tcg cac acc ctg gac caa gtc aat cgc acc cac ttc cct ttc ttc 278
Pro Ser His Thr Leu Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe
15 20 25

tcg gat gtc aag ggc gac cac cgg ttg gtg ttg agc gtc gtg gag acc 326
Ser Asp Val Lys Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr
30 35 40

acc gtt ctg gga ctc atc ttt gtc gtc tca ctg ctg ggc aac gtg tgt 374
Thr Val Leu Gly Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys
45 50 55 60

gct cta gtg ctg gtg gcg cgc cgt cgg cgc cgt ggg gcg tca gcc agc 422

Ala Leu Val Leu Val Ala Arg Arg Arg Arg Gly Ala Ser Ala Ser		
65	70	75
ctg gtg ctc aac ctc ttc tgc gcg gat ttg ctc ttc acc agc gcc atc		470
Leu Val Leu Asn Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile		
80	85	90
cct cta gtg ctc gtc gtg cgc tgg act gag gcc tgg ctg ttg ggg ccc		518
Pro Leu Val Leu Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro		
95	100	105
gtc gtc tgc cac ctg ctc ttc tac gtg atg aca atg agc ggc agc gtc		566
Val Val Cys His Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val		
110	115	120
acg atc ctc aca ctg gcc gcg gtc agc ctg gag cgc atg gtg tgc atc		614
Thr Ile Leu Thr Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile		
125	130	135
140		
gtg cgc ctc cgg cgc ggc ttg agc ggc ccg ggg cgg cgg act cag gcg		662
Val Arg Leu Arg Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala		
145	150	155
gca ctg ctg gct ttc ata tgg ggt tac tcg gcg ctc gcc gcg ctg ccc		710
Ala Leu Leu Ala Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro		
160	165	170
ctc tac atc ttg ttc cgc gtg gtc ccg cag cgc ctt ccc ggc ggg gac		758
Leu Tyr Ile Leu Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp		
175	180	185
cag gaa att ccg att tgc aca ttg gat tgg ccc aac cgc ata gga gaa		806
Gln Glu Ile Pro Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu		
190	195	200
atc tca tgg gat gtg ttt ttt gag act ttg aac ttc ctg gtg ccg gga		854
Ile Ser Trp Asp Val Phe Phe Glu Thr Leu Asn Phe Leu Val Pro Gly		
205	210	215
220		
ctg gtc att gtg atc agt tac tcc aaa att tta cag atc acg aaa gca		902
Leu Val Ile Val Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala		
225	230	235
tcg cgg aag agg ctt acg ctg agc ttg gca tac tct gag agc cac cag		950
Ser Arg Lys Arg Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln		
240	245	250
atc cga gtg tcc caa caa gac tac cga ctc ttc cgc acg ctc ttc ctg		998
Ile Arg Val Ser Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu		
255	260	265
ctc atg gtt tcc ttc atc atg tgg agt ccc atc atc atc acc atc		1046
Leu Met Val Ser Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile		
270	275	280
ctc ctc atc ttg atc caa aac ttc cgg cag gac ctg gtc atc tgg cca		1094
Leu Leu Ile Leu Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro		
285	290	295
300		
tcc ctt ttc ttc tgg gtg gtg gcc ttc acg ttt gcc aac tct gcc cta		1142
Ser Leu Phe Phe Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu		

305

310

315

aac ccc ata ctg tac aac atg tcg ctg ttc agg aac gaa tgg agg aag	1190
Asn Pro Ile Leu Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys	
320	325
	330

att ttt tgc tgc ttc ttt cca gag aag gga gcc att ttt aca gat	1238
Ile Phe Cys Cys Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp	
335	340
	345

acg tct gtc agg cga aat gac ttg tct gtt att tcc agc taa	1280
Thr Ser Val Arg Arg Asn Asp Leu Ser Val Ile Ser Ser *	
350	355
	360

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gcccaccagt gcgcctcgct ttaaaaatac ccgacttcca acagcaggca tctacggagc 1400	
cagcaaatta aggaatgatc gctcagttata aaaatatttt tccttaaaag aactttctat 1460	
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attataacg tgccctaca aaaaaaaaaaaaaaaa 1560	

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<211> 361

<212> PRT

<213> Murine ortholog

<400> 5

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20 25 30	

Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr Thr Val Leu Gly	
35 40 45	

Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu	
50 55 60	

Val Ala Arg Arg Arg Arg Gly Ala Ser Ala Ser Leu Val Leu Asn	
65 70 75 80	

Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu	
85 90 95	

Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His	
100 105 110	

Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr	
115 120 125	

Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg	
130 135 140	

Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala	
145 150 155 160	

Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Tyr Ile Leu	
165 170 175	

Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro	
180 185 190	

Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp	
195 200 205	

Val Phe Phe Glu Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val	
210 215 220	

Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg	
225 230 235 240	

Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser	
245 250 255	

Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser	
260 265 270	

Phe Phe Ile Met Trp Ser Pro Ile Ile Thr Ile Leu Ile Leu	
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275	280	285
Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser	Leu Phe Phe	
290	295	300
Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala	Leu Asn Pro Ile	Leu
305	310	315
Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile	Phe Cys Cys	
325	330	335
Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp Thr	Ser Val Arg	
340	345	350
Arg Asn Asp Leu Ser Val Ile Ser Ser		
355	360	

<210> 6
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<212> DNA
<213> Murine ortholog

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gtcggtggaga ccaccgttct gggactcatc tttgtcgatct cactgctggg caacgtgtgt 180
gctctagtgc tggtggcgcg ccgtcgccgc cgtggggcgt cagccagcct ggtgctcaac 240
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agccgcagcg tcacgatcc cacactggcc gcggtcagcc tggagcgcatt ggtgtgcata 420
gtgcgcctcc ggcgcggctt gagcggcccg gggccggcga ctcaaggcgcc actgctggct 480
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ccgcagcgcc ttcccgccgg ggaccaggaa attccgattt gcacatttggaa ttggcccaac 600
cgcataggag aaatctcatg ggatgtgttt tttgagactt tgaacttccct ggtgcgggaa 660
ctggtcattt tggatcgatc ttccaaaattt ttacagatca cgaaagcata cgccaaagagg 720
cttacgctga gcttggcata ctctgagagc caccagatcc gagtgtccca acaagactac 780
cgactcttcc gcacgcctt cctgctcatg gtttcccttc tcatcatgtg gagtccccatc 840
atcatcacca tcctccatcat cttgatccaa aacttccggc aggacctggt catctggcca 900
tccctttct tctgggtggt ggccttcacg tttgccaact ctgccttaaa cccctatactg 960
tacaacatgt cgctgttcag gaacgaatgg aggaagattt tttgctgtttt cttttttcca 1020
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agctaa 1086

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<212> DNA
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<400> 7
acttcaagga aagcccacca 20

<210> 8
<211> 20
<212> DNA
<213> Murine ortholog

<400> 8
tccgttagatg cctgctgttg 20

<210> 9
<211> 27
<212> DNA
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<400> 9

tgcgccctgc tttaaaaata cccgact 27
<210> 10
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<212> DNA
<213> Homo sapiens

<400> 10
acctgggagg cagaggttg 19

<210> 11
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tcttgttgccttg 20

<210> 12
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<400> 12
agttagccga gatcgtgcca ttgc 24

<210> 13
<211> 21
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<213> Homo sapiens

<400> 13
gcgcggaa tgtccccctga a 21

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ttgtcgatta tttctggcta a 21

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<400> 15
ccgggcatgt cccctgag 18

<210> 16
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tctgttattt ccagctaa 18